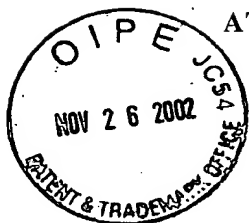


amat B

ATTORNEY DOCKET NO. 14014.0323U3



SEQUENCE LISTING

<110> Chiorini, John
Kotin, Robert M.
Safer, Brian

<120> AAV5 VECTOR AND USES THEREOF

<130> 14014.0323U3

<140> 09/717,789

<141> 2000-11-21

<150> PCT/US99/11958

<151> 1999-05-28

<150> 60/087,029

<151> 1998-05-28

<160> 24

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 4652

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =
synthetic construct

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tgtcataatg	atgtaatgct	tattgtcacg	cgatagttaa	tgattaacag	tcattgtgatg	240
tgttttatcc	aataggaaga	aagcgcgctg	atgagttctc	gcgagacttc	cggggtataa	300
aagaccgagt	gaacgagccc	gcgcgccattc	tttgctctgg	actgctagag	gaccctcgct	360
gccatggcta	ccttctatga	agtcattggt	cgcgtcccat	ttgacgtgga	ggaacatctg	420
cctggaattt	ctgacagctt	tgtggactgg	gtaactggtc	aaatttggga	gctgcctcca	480
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cgccgcgtgt	tcctgtacga	gtggaacaaa	ttttccaagc	aggagtccaa	attctttgtg	600
cagtttgaaa	agggatctga	atattttcat	ctgcacacgc	ttgtggagac	ctccggcatc	660
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ATTORNEY DOCKET NO. 14014.0323U3

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<210> 2
 <211> 390
 <212> PRT
 <213> Artificial Sequence

ATTORNEY DOCKET NO. 14014.0323U3

<220>

<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 2

Met	Ala	Leu	Val	Asn	Trp	Leu	Val	Glu	His	Gly	Ile	Thr	Ser	Glu	Lys
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Gln	Trp	Ile	Gln	Glu	Asn	Gln	Glu	Ser	Tyr	Leu	Ser	Phe	Asn	Ser	Thr
			20					25					30		
Gly	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Thr	Lys
	35						40					45			
Ile	Met	Ser	Leu	Thr	Lys	Ser	Ala	Val	Asp	Tyr	Leu	Val	Gly	Ser	Ser
	50					55					60				
Val	Pro	Glu	Asp	Ile	Ser	Lys	Asn	Arg	Ile	Trp	Gln	Ile	Phe	Glu	Met
65					70				75					80	
Asn	Gly	Tyr	Asp	Pro	Ala	Tyr	Ala	Gly	Ser	Ile	Leu	Tyr	Gly	Trp	Cys
				85				90						95	
Gln	Arg	Ser	Phe	Asn	Lys	Arg	Asn	Thr	Val	Trp	Leu	Tyr	Gly	Pro	Ala
			100					105					110		
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
		115					120					125			
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
	130					135					140				
Cys	Val	Asp	Lys	Met	Leu	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Asn
145					150					155					160
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
				165					170					175	
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Val	Gln	Ile	Asp	Ser	Thr	Pro	Val
			180					185					190		
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Val	Val	Val	Asp	Gly	Asn	Ser
	195					200						205			
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Glu	Asp	Arg	Met	Phe	Lys	Phe
	210				215						220				
Glu	Leu	Thr	Lys	Arg	Leu	Pro	Pro	Asp	Phe	Gly	Lys	Ile	Thr	Lys	Gln
225					230					235					240
Glu	Val	Lys	Asp	Phe	Phe	Ala	Trp	Ala	Lys	Val	Asn	Gln	Val	Pro	Val
				245					250					255	
Thr	His	Glu	Phe	Lys	Val	Pro	Arg	Glu	Leu	Ala	Gly	Thr	Lys	Gly	Ala
			260					265					270		
Glu	Lys	Ser	Leu	Lys	Arg	Pro	Leu	Gly	Asp	Val	Thr	Asn	Thr	Ser	Tyr
	275						280					285			
Lys	Ser	Leu	Glu	Lys	Arg	Ala	Arg	Leu	Ser	Phe	Val	Pro	Glu	Thr	Pro
	290					295					300				
Arg	Ser	Ser	Asp	Val	Thr	Val	Asp	Pro	Ala	Pro	Leu	Arg	Pro	Leu	Asn
305					310					315					320
Trp	Asn	Ser	Arg	Tyr	Asp	Cys	Lys	Cys	Asp	Tyr	His	Ala	Gln	Phe	Asp
				325					330					335	
Asn	Ile	Ser	Asn	Lys	Cys	Asp	Glu	Cys	Glu	Tyr	Leu	Asn	Arg	Gly	Lys
			340					345					350		
Asn	Gly	Cys	Ile	Cys	His	Asn	Val	Thr	His	Cys	Gln	Ile	Cys	His	Gly
	355						360					365			
Ile	Pro	Pro	Trp	Glu	Lys	Glu	Asn	Leu	Ser	Asp	Phe	Gly	Asp	Phe	Asp
	370					375						380			
Asp	Ala	Asn	Lys	Glu	Gln										
385					390										

<210> 3

<211> 610

<212> PRT

<213> Artificial Sequence

ATTORNEY DOCKET NO. 14014.0323U3

<220>

<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 3

Met	Ala	Thr	Phe	Tyr	Glu	Val	Ile	Val	Arg	Val	Pro	Phe	Asp	Val	Glu
1				5					10					15	
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asp	Trp	Val	Thr	Gly
			20					25					30		
Gln	Ile	Trp	Glu	Leu	Pro	Pro	Glu	Ser	Asp	Leu	Asn	Leu	Thr	Leu	Val
		35					40					45			
Glu	Gln	Pro	Gln	Leu	Thr	Val	Ala	Asp	Arg	Ile	Arg	Arg	Val	Phe	Leu
	50					55					60				
Tyr	Glu	Trp	Asn	Lys	Phe	Ser	Lys	Gln	Glu	Ser	Lys	Phe	Phe	Val	Gln
65				70						75					80
Phe	Glu	Lys	Gly	Ser	Glu	Tyr	Phe	His	Leu	His	Thr	Leu	Val	Glu	Thr
				85					90					95	
Ser	Gly	Ile	Ser	Ser	Met	Val	Leu	Gly	Arg	Tyr	Val	Ser	Gln	Ile	Arg
			100					105					110		
Ala	Gln	Leu	Val	Lys	Val	Val	Phe	Gln	Gly	Ile	Glu	Pro	Gln	Ile	Asn
		115					120					125			
Asp	Trp	Val	Ala	Ile	Thr	Lys	Val	Lys	Lys	Gly	Gly	Ala	Asn	Lys	Val
	130					135					140				
Val	Asp	Ser	Gly	Tyr	Ile	Pro	Ala	Tyr	Leu	Leu	Pro	Lys	Val	Gln	Pro
145					150					155					160
Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Leu	Asp	Glu	Tyr	Lys	Leu	Ala	Ala
			165					170					175		
Leu	Asn	Leu	Glu	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	Phe	Leu	Ala	Glu
			180					185					190		
Ser	Ser	Gln	Arg	Ser	Gln	Glu	Ala	Ala	Ser	Gln	Arg	Glu	Phe	Ser	Ala
		195				200						205			
Asp	Pro	Val	Ile	Lys	Ser	Lys	Thr	Ser	Gln	Lys	Tyr	Met	Ala	Leu	Val
	210					215					220				
Asn	Trp	Leu	Val	Glu	His	Gly	Ile	Thr	Ser	Glu	Lys	Gln	Trp	Ile	Gln
225					230					235					240
Glu	Asn	Gln	Glu	Ser	Tyr	Leu	Ser	Phe	Asn	Ser	Thr	Gly	Asn	Ser	Arg
			245						250				255		
Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Thr	Lys	Ile	Met	Ser	Leu
		260						265					270		
Thr	Lys	Ser	Ala	Val	Asp	Tyr	Leu	Val	Gly	Ser	Ser	Val	Pro	Glu	Asp
		275					280					285			
Ile	Ser	Lys	Asn	Arg	Ile	Trp	Gln	Ile	Phe	Glu	Met	Asn	Gly	Tyr	Asp
	290					295					300				
Pro	Ala	Tyr	Ala	Gly	Ser	Ile	Leu	Tyr	Gly	Trp	Cys	Gln	Arg	Ser	Phe
305				310						315					320
Asn	Lys	Arg	Asn	Thr	Val	Trp	Leu	Tyr	Gly	Pro	Ala	Thr	Thr	Gly	Lys
			325						330					335	
Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro	Phe	Tyr	Gly	Cys
		340						345					350		
Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp	Cys	Val	Asp	Lys
		355					360					365			
Met	Leu	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Asn	Lys	Val	Val	Glu
	370					375					380				
Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg	Val	Asp	Gln	Lys
385					390					395					400
Cys	Lys	Ser	Ser	Val	Gln	Ile	Asp	Ser	Thr	Pro	Val	Ile	Val	Thr	Ser
			405						410					415	
Asn	Thr	Asn	Met	Cys	Val	Val	Val	Asp	Gly	Asn	Ser	Thr	Thr	Phe	Glu
			420					425					430		

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His Gln Gln Pro Leu Glu Asp Arg Met Phe Lys Phe Glu Leu Thr Lys
 435 440 445
 Arg Leu Pro Pro Asp Phe Gly Lys Ile Thr Lys Gln Glu Val Lys Asp
 450 455 460
 Phe Phe Ala Trp Ala Lys Val Asn Gln Val Pro Val Thr His Glu Phe
 465 470 475 480
 Lys Val Pro Arg Glu Leu Ala Gly Thr Lys Gly Ala Glu Lys Ser Leu
 485 490 495
 Lys Arg Pro Leu Gly Asp Val Thr Asn Thr Ser Tyr Lys Ser Leu Glu
 500 505 510
 Lys Arg Ala Arg Leu Ser Phe Val Pro Glu Thr Pro Arg Ser Ser Asp
 515 520 525
 Val Thr Val Asp Pro Ala Pro Leu Arg Pro Leu Asn Trp Asn Ser Arg
 530 535 540
 Tyr Asp Cys Lys Cys Asp Tyr His Ala Gln Phe Asp Asn Ile Ser Asn
 545 550 555 560
 Lys Cys Asp Glu Cys Glu Tyr Leu Asn Arg Gly Lys Asn Gly Cys Ile
 565 570 575
 Cys His Asn Val Thr His Cys Gln Ile Cys His Gly Ile Pro Pro Trp
 580 585 590
 Glu Lys Glu Asn Leu Ser Asp Phe Gly Asp Phe Asp Asp Ala Asn Lys
 595 600 605
 Glu Gln
 610

<210> 4
 <211> 724
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/Note =
 synthetic construct

<400> 4
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 Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
 20 25 30
 Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
 35 40 45
 Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
 50 55 60
 Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
 65 70 75 80
 Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
 85 90 95
 Ala Glu Phe Gln Glu Lys Leu Ala Asp Thr Ser Phe Gly Gly Asn
 100 105 110
 Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
 115 120 125
 Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
 130 135 140
 Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
 145 150 155 160
 Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
 165 170 175
 Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
 180 185 190
 Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
 195 200 205

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Asp	Gly	Val	Gly	Asn	Ala	Ser	Gly	Asp	Trp	His	Cys	Asp	Ser	Thr	Trp
210						215					220				
Met	Gly	Asp	Arg	Val	Val	Thr	Lys	Ser	Thr	Arg	Thr	Trp	Val	Leu	Pro
225					230					235					240
Ser	Tyr	Asn	Asn	His	Gln	Tyr	Arg	Glu	Ile	Lys	Ser	Gly	Ser	Val	Asp
				245					250					255	
Gly	Ser	Asn	Ala	Asn	Ala	Tyr	Phe	Gly	Tyr	Ser	Thr	Pro	Trp	Gly	Tyr
			260					265					270		
Phe	Asp	Phe	Asn	Arg	Phe	His	Ser	His	Trp	Ser	Pro	Arg	Asp	Trp	Gln
			275				280					285			
Arg	Leu	Ile	Asn	Asn	Tyr	Trp	Gly	Phe	Arg	Pro	Arg	Ser	Leu	Arg	Val
						295					300				
Lys	Ile	Phe	Asn	Ile	Gln	Val	Lys	Glu	Val	Thr	Val	Gln	Asp	Ser	Thr
305					310					315					320
Thr	Thr	Ile	Ala	Asn	Asn	Leu	Thr	Ser	Thr	Val	Gln	Val	Phe	Thr	Asp
				325					330					335	
Asp	Asp	Tyr	Gln	Leu	Pro	Tyr	Val	Val	Gly	Asn	Gly	Thr	Glu	Gly	Cys
			340					345					350		
Leu	Pro	Ala	Phe	Pro	Pro	Gln	Val	Phe	Thr	Leu	Pro	Gln	Tyr	Gly	Tyr
		355					360					365			
Ala	Thr	Leu	Asn	Arg	Asp	Asn	Thr	Glu	Asn	Pro	Thr	Glu	Arg	Ser	Ser
					375						380				
Phe	Phe	Cys	Leu	Glu	Tyr	Phe	Pro	Ser	Lys	Met	Leu	Arg	Thr	Gly	Asn
385					390					395					400
Asn	Phe	Glu	Phe	Thr	Tyr	Asn	Phe	Glu	Glu	Val	Pro	Phe	His	Ser	Ser
				405					410					415	
Phe	Ala	Pro	Ser	Gln	Asn	Leu	Phe	Lys	Leu	Ala	Asn	Pro	Leu	Val	Asp
			420					425					430		
Gln	Tyr	Leu	Tyr	Arg	Phe	Val	Ser	Thr	Asn	Asn	Thr	Gly	Gly	Val	Gln
			435					440					445		
Phe	Asn	Lys	Asn	Leu	Ala	Gly	Arg	Tyr	Ala	Asn	Thr	Tyr	Lys	Asn	Trp
						455					460				
Phe	Pro	Gly	Pro	Met	Gly	Arg	Thr	Gln	Gly	Trp	Asn	Leu	Gly	Ser	Gly
465					470					475					480
Val	Asn	Arg	Ala	Ser	Val	Ser	Ala	Phe	Ala	Thr	Thr	Asn	Arg	Met	Glu
				485					490					495	
Leu	Glu	Gly	Ala	Ser	Tyr	Gln	Val	Pro	Pro	Gln	Pro	Asn	Gly	Met	Thr
			500					505					510		
Asn	Asn	Leu	Gln	Gly	Ser	Asn	Thr	Tyr	Ala	Leu	Glu	Asn	Thr	Met	Ile
			515				520					525			
Phe	Asn	Ser	Gln	Pro	Ala	Asn	Pro	Gly	Thr	Thr	Ala	Thr	Tyr	Leu	Glu
					535						540				
Gly	Asn	Met	Leu	Ile	Thr	Ser	Glu	Ser	Glu	Thr	Gln	Pro	Val	Asn	Arg
545					550					555					560
Val	Ala	Tyr	Asn	Val	Gly	Gly	Gln	Met	Ala	Thr	Asn	Asn	Gln	Ser	Ser
				565					570					575	
Thr	Thr	Ala	Pro	Ala	Thr	Gly	Thr	Tyr	Asn	Leu	Gln	Glu	Ile	Val	Pro
			580					585					590		
Gly	Ser	Val	Trp	Met	Glu	Arg	Asp	Val	Tyr	Leu	Gln	Gly	Pro	Ile	Trp
			595				600					605			
Ala	Lys	Ile	Pro	Glu	Thr	Gly	Ala	His	Phe	His	Pro	Ser	Pro	Ala	Met
					615						620				
Gly	Gly	Phe	Gly	Leu	Lys	His	Pro	Pro	Pro	Met	Met	Leu	Ile	Lys	Asn
625					630					635					640
Thr	Pro	Val	Pro	Gly	Asn	Ile	Thr	Ser	Phe	Ser	Asp	Val	Pro	Val	Ser
				645					650					655	
Ser	Phe	Ile	Thr	Gln	Tyr	Ser	Thr	Gly	Gln	Val	Thr	Val	Glu	Met	Glu
			660					665					670		
Trp	Glu	Leu	Lys	Lys	Glu	Asn	Ser	Lys	Arg	Trp	Asn	Pro	Glu	Ile	Gln
			675				680					685			

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Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
690 695 700
Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705 710 715 720
Thr Arg Pro Leu

<210> 5
<211> 588
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 5
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Lys Ala Arg Thr Glu Glu Asp Ser Lys Pro Ser Thr Ser Ser Asp Ala
20 25 30
Glu Ala Gly Pro Ser Gly Ser Gln Gln Leu Gln Ile Pro Ala Gln Pro
35 40 45
Ala Ser Ser Leu Gly Ala Asp Thr Met Ser Ala Gly Gly Gly Gly Pro
50 55 60
Leu Gly Asp Asn Asn Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly
65 70 75 80
Asp Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Val Thr Lys
85 90 95
Ser Thr Arg Thr Trp Val Leu Pro Ser Tyr Asn Asn His Gln Tyr Arg
100 105 110
Glu Ile Lys Ser Gly Ser Val Asp Gly Ser Asn Ala Asn Ala Tyr Phe
115 120 125
Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Ser
130 135 140
His Trp Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Tyr Trp Gly
145 150 155 160
Phe Arg Pro Arg Ser Leu Arg Val Lys Ile Phe Asn Ile Gln Val Lys
165 170 175
Glu Val Thr Val Gln Asp Ser Thr Thr Thr Ile Ala Asn Asn Leu Thr
180 185 190
Ser Thr Val Gln Val Phe Thr Asp Asp Asp Tyr Gln Leu Pro Tyr Val
195 200 205
Val Gly Asn Gly Thr Glu Gly Cys Leu Pro Ala Phe Pro Pro Gln Val
210 215 220
Phe Thr Leu Pro Gln Tyr Gly Tyr Ala Thr Leu Asn Arg Asp Asn Thr
225 230 235 240
Glu Asn Pro Thr Glu Arg Ser Ser Phe Phe Cys Leu Glu Tyr Phe Pro
245 250 255
Ser Lys Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Thr Tyr Asn Phe
260 265 270
Glu Glu Val Pro Phe His Ser Ser Phe Ala Pro Ser Gln Asn Leu Phe
275 280 285
Lys Leu Ala Asn Pro Leu Val Asp Gln Tyr Leu Tyr Arg Phe Val Ser
290 295 300
Thr Asn Asn Thr Gly Gly Val Gln Phe Asn Lys Asn Leu Ala Gly Arg
305 310 315 320
Tyr Ala Asn Thr Tyr Lys Asn Trp Phe Pro Gly Pro Met Gly Arg Thr
325 330 335
Gln Gly Trp Asn Leu Gly Ser Gly Val Asn Arg Ala Ser Val Ser Ala
340 345 350

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Phe	Ala	Thr	Thr	Asn	Arg	Met	Glu	Leu	Glu	Gly	Ala	Ser	Tyr	Gln	Val
		355					360					365			
Pro	Pro	Gln	Pro	Asn	Gly	Met	Thr	Asn	Asn	Leu	Gln	Gly	Ser	Asn	Thr
		370				375					380				
Tyr	Ala	Leu	Glu	Asn	Thr	Met	Ile	Phe	Asn	Ser	Gln	Pro	Ala	Asn	Pro
385					390					395					400
Gly	Thr	Thr	Ala	Thr	Tyr	Leu	Glu	Gly	Asn	Met	Leu	Ile	Thr	Ser	Glu
				405					410					415	
Ser	Glu	Thr	Gln	Pro	Val	Asn	Arg	Val	Ala	Tyr	Asn	Val	Gly	Gly	Gln
			420					425					430		
Met	Ala	Thr	Asn	Asn	Gln	Ser	Ser	Thr	Thr	Ala	Pro	Ala	Thr	Gly	Thr
		435					440					445			
Tyr	Asn	Leu	Gln	Glu	Ile	Val	Pro	Gly	Ser	Val	Trp	Met	Glu	Arg	Asp
		450				455					460				
Val	Tyr	Leu	Gln	Gly	Pro	Ile	Trp	Ala	Lys	Ile	Pro	Glu	Thr	Gly	Ala
465					470					475					480
His	Phe	His	Pro	Ser	Pro	Ala	Met	Gly	Gly	Phe	Gly	Leu	Lys	His	Pro
				485					490					495	
Pro	Pro	Met	Met	Leu	Ile	Lys	Asn	Thr	Pro	Val	Pro	Gly	Asn	Ile	Thr
			500					505					510		
Ser	Phe	Ser	Asp	Val	Pro	Val	Ser	Ser	Phe	Ile	Thr	Gln	Tyr	Ser	Thr
		515					520					525			
Gly	Gln	Val	Thr	Val	Glu	Met	Glu	Trp	Glu	Leu	Lys	Lys	Glu	Asn	Ser
		530				535					540				
Lys	Arg	Trp	Asn	Pro	Glu	Ile	Gln	Tyr	Thr	Asn	Asn	Tyr	Asn	Asp	Pro
545					550					555					560
Gln	Phe	Val	Asp	Phe	Ala	Pro	Asp	Ser	Thr	Gly	Glu	Tyr	Arg	Thr	Thr
				565					570					575	
Arg	Pro	Ile	Gly	Thr	Arg	Tyr	Leu	Thr	Arg	Pro	Leu				
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<210> 6

<211> 532

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 6

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Asp	Gly	Val	Gly	Asn	Ala	Ser	Gly	Asp	Trp	His	Cys	Asp	Ser	Thr	Trp
			20					25					30		
Met	Gly	Asp	Arg	Val	Val	Thr	Lys	Ser	Thr	Arg	Thr	Trp	Val	Leu	Pro
		35					40					45			
Ser	Tyr	Asn	Asn	His	Gln	Tyr	Arg	Glu	Ile	Lys	Ser	Gly	Ser	Val	Asp
		50				55					60				
Gly	Ser	Asn	Ala	Asn	Ala	Tyr	Phe	Gly	Tyr	Ser	Thr	Pro	Trp	Gly	Tyr
65					70					75					80
Phe	Asp	Phe	Asn	Arg	Phe	His	Ser	His	Trp	Ser	Pro	Arg	Asp	Trp	Gln
			85						90					95	
Arg	Leu	Ile	Asn	Asn	Tyr	Trp	Gly	Phe	Arg	Pro	Arg	Ser	Leu	Arg	Val
			100					105					110		
Lys	Ile	Phe	Asn	Ile	Gln	Val	Lys	Glu	Val	Thr	Val	Gln	Asp	Ser	Thr
		115					120					125			
Thr	Thr	Ile	Ala	Asn	Asn	Leu	Thr	Ser	Thr	Val	Gln	Val	Phe	Thr	Asp
		130				135					140				
Asp	Asp	Tyr	Gln	Leu	Pro	Tyr	Val	Val	Gly	Asn	Gly	Thr	Glu	Gly	Cys
145					150					155					160

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Leu	Pro	Ala	Phe	Pro	Pro	Gln	Val	Phe	Thr	Leu	Pro	Gln	Tyr	Gly	Tyr
				165					170					175	
Ala	Thr	Leu	Asn	Arg	Asp	Asn	Thr	Glu	Asn	Pro	Thr	Glu	Arg	Ser	Ser
			180					185					190		
Phe	Phe	Cys	Leu	Glu	Tyr	Phe	Pro	Ser	Lys	Met	Leu	Arg	Thr	Gly	Asn
		195					200					205			
Asn	Phe	Glu	Phe	Thr	Tyr	Asn	Phe	Glu	Glu	Val	Pro	Phe	His	Ser	Ser
	210					215					220				
Phe	Ala	Pro	Ser	Gln	Asn	Leu	Phe	Lys	Leu	Ala	Asn	Pro	Leu	Val	Asp
225					230					235					240
Gln	Tyr	Leu	Tyr	Arg	Phe	Val	Ser	Thr	Asn	Thr	Gly	Gly	Val	Gln	
				245					250				255		
Phe	Asn	Lys	Asn	Leu	Ala	Gly	Arg	Tyr	Ala	Asn	Thr	Tyr	Lys	Asn	Trp
			260					265					270		
Phe	Pro	Gly	Pro	Met	Gly	Arg	Thr	Gln	Gly	Trp	Asn	Leu	Gly	Ser	Gly
		275					280					285			
Val	Asn	Arg	Ala	Ser	Val	Ser	Ala	Phe	Ala	Thr	Thr	Asn	Arg	Met	Glu
	290					295					300				
Leu	Glu	Gly	Ala	Ser	Tyr	Gln	Val	Pro	Pro	Gln	Pro	Asn	Gly	Met	Thr
305					310					315					320
Asn	Asn	Leu	Gln	Gly	Ser	Asn	Thr	Tyr	Ala	Leu	Glu	Asn	Thr	Met	Ile
			325						330					335	
Phe	Asn	Ser	Gln	Pro	Ala	Asn	Pro	Gly	Thr	Thr	Ala	Thr	Tyr	Leu	Glu
			340					345					350		
Gly	Asn	Met	Leu	Ile	Thr	Ser	Glu	Ser	Glu	Thr	Gln	Pro	Val	Asn	Arg
		355					360				365				
Val	Ala	Tyr	Asn	Val	Gly	Gly	Gln	Met	Ala	Thr	Asn	Asn	Gln	Ser	Ser
	370					375					380				
Thr	Thr	Ala	Pro	Ala	Thr	Gly	Thr	Tyr	Asn	Leu	Gln	Glu	Ile	Val	Pro
385					390					395					400
Gly	Ser	Val	Trp	Met	Glu	Arg	Asp	Val	Tyr	Leu	Gln	Gly	Pro	Ile	Trp
			405						410					415	
Ala	Lys	Ile	Pro	Glu	Thr	Gly	Ala	His	Phe	His	Pro	Ser	Pro	Ala	Met
			420					425					430		
Gly	Gly	Phe	Gly	Leu	Lys	His	Pro	Pro	Pro	Met	Met	Leu	Ile	Lys	Asn
		435					440					445			
Thr	Pro	Val	Pro	Gly	Asn	Ile	Thr	Ser	Phe	Ser	Asp	Val	Pro	Val	Ser
	450					455					460				
Ser	Phe	Ile	Thr	Gln	Tyr	Ser	Thr	Gly	Gln	Val	Thr	Val	Glu	Met	Glu
465					470					475					480
Trp	Glu	Leu	Lys	Lys	Glu	Asn	Ser	Lys	Arg	Trp	Asn	Pro	Glu	Ile	Gln
			485						490					495	
Tyr	Thr	Asn	Asn	Tyr	Asn	Asp	Pro	Gln	Phe	Val	Asp	Phe	Ala	Pro	Asp
			500					505					510		
Ser	Thr	Gly	Glu	Tyr	Arg	Thr	Thr	Arg	Pro	Ile	Gly	Thr	Arg	Tyr	Leu
		515					520					525			
Thr	Arg	Pro	Leu												
			530												

<210> 7
 <211> 2307
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/Note =
 synthetic construct

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accctccaga	ttggttggaa	gaagttggtg	aaggtcttcg	cgagtttttg	ggccttgaag	180
cgggcccacc	gaaacccaaa	cccaatcagc	agcatcaaga	tcaagcccgt	ggtcttgtgc	240
tgcttggtta	taactatctc	ggaccgcgaa	acggtctcga	tcgaggagag	cctgtcaaca	300
gggcagacga	ggtcgcgcga	gagcacgaca	tctcgtacaa	cgagcagctt	gaggcgggag	360
acaaccccta	cctcaagtac	aaccacgcgg	acgccgagtt	tcaggagaag	ctcgccgacg	420
acacatcctt	cgggggaaac	ctcggaaagg	cagtctttca	ggccaagaaa	aggggttctcg	480
aaccttttgg	cctggttgaa	gaggggtgcta	agacggcccc	taccgaaaag	cggatagacg	540
accactttcc	aaaaagaaaag	aaggctcggg	ccgaagagga	ctccaagcct	tccacctcgt	600
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caagtttggg	agctgataca	atgtctgcgg	gaggtggcgg	cccattgggc	gacaataacc	720
aaggtgccga	tggagtgggc	aatgcctcgg	gagattggca	ttgcgattcc	acgtggatgg	780
gggacagagt	cgtcaccaag	tccacccgaa	cctgggtgct	gcccagctac	aacaaccacc	840
agtaccgaga	gatcaaaaag	ggctccgtcg	acggaaagcaa	cgccaacgcc	tactttggat	900
acagcacccc	ctgggggtac	tttgacttta	accgcttcca	cagccactgg	agcccccgag	960
actggcaaaag	actcatcaac	aactactggg	gcttcagacc	ccggtcccctc	agagtcaaaa	1020
tcttcaacat	tcaagtcaaa	gaggtcacgg	tgcaggactc	caccaccacc	atcgccaaca	1080
acctcacctc	caccgtccaa	gtgtttacgg	acgacgacta	ccagctgccc	tacgtcgtcg	1140
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acgggttacgc	gacgctgaac	cgcgacaaca	cagaaaatcc	caccgagagg	agcagcttct	1260
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acaactttga	ggaggtgccc	ttccactcca	gcttcgctcc	cagtcagaac	ctgttcaagc	1380
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gagtccagtt	caacaagaac	ctggccggga	gatacgccaa	cacctacaaa	aactggttcc	1500
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tcagcgcctt	cgccacgacc	aataggatgg	agctcgaggg	cgcgagttac	caggtgcccc	1620
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ccatctgggc	caagatccca	gagacggggg	cgcaactttca	cccctctccg	gccatggggcg	1980
gattcggact	caaacaccca	ccgcccataga	tgctcatcaa	gaacacgcct	gtgcccggaa	2040
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aggtcaccgt	ggagatggag	tgggagctca	agaaggaaaa	ctccaagagg	tggaaaccag	2160
agatccagta	cacaaacaac	tacaacgacc	cccagtttgt	ggactttgcc	ccggacagca	2220
ccggggaata	cagaaccacc	agacctatcg	gaacccgata	ccttacccca	cccctttaac	2280
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<210> 8
 <211> 2264
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/Note =
 synthetic construct

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gtttttgggc	cttgaagcgg	gccacccgaa	acaaaaaccc	aatcagcagc	atcaagatca	180
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ggagaagctc	gccgacgaca	catccttcgg	gggaaacctc	ggaaaggcag	tctttcaggc	420
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attggggcag	aataaccaag	gtgccgatgg	agtgggcaat	gcctcgggag	attggcattg	720
cgattccacg	tggatggggg	acagagtcgt	caccaagtc	acccgaacct	gggtgctgcc	780

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cagctacaac	aaccaccagt	accgagagat	caaaagcggc	tccgtcgacg	gaagcaacgc	840
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ccactggagc	ccccgagact	ggcaaagact	catcaacaac	tactgggggt	tcagaccccg	960
gtccctcaga	gtcaaaatct	tcaacattca	agtcaaagag	gtcacgggtgc	aggactccac	1020
caccaccatc	gccaacaacc	tcacctccac	cgtccaagtg	tttacggacg	acgactacca	1080
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ctttacgctg	ccgcagtagc	gttacgcgac	gctgaaccgc	gacaacacag	aaaatcccac	1200
cgagaggagc	agcttcttct	gcctagagta	ctttcccagc	aagatgctga	gaacgggcaa	1260
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ctacaaaaac	tgggttcccgg	ggcccatggg	ccgaaccag	ggctggaacc	tgggtcccgg	1500
ggtcaaccgc	gccagtgta	gcgccttcgc	cacgaccaat	aggatggagc	tcgagggcgc	1560
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cacgcctgtg	cccggaaata	tcaccagctt	ctcggagctg	cccgtcagca	gcttcatcac	2040
ccagtacagc	accgggcagg	taccgtgga	gatggagtgg	gagctcaaga	aggaaaactc	2100
caagaggtgg	aaccagaga	tccagtacac	aaacaactac	aacgaccccc	agtttgtgga	2160
ctttgccccg	gacagcaccg	gggaatacag	aaccaccaga	cctatcgga	cccgatacct	2220
taccgcaccc	ctttaaccca	ttcatgtcgc	ataccctcaa	taaa		2264

<210> 9

<211> 2264

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 9

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gtttttgggc	cttgaagcgg	gcccaccgaa	acaaaaaccc	aatcagcagc	atcaagatca	180
agcccggtgt	cttgtctgc	ctgggtataa	ctatctcgga	cccggaaacg	gtctcgatcg	240
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gcagcttgag	gcgggagaca	acccctacct	caagtacaac	cacgcggacg	ccgagtttca	360
ggagaagctc	gccgacgaca	catccttcgg	gggaaacctc	ggaaaggcag	tcttttcaggc	420
caagaaaagg	gttctcgaac	cttttggcct	ggttgaagag	ggtgctaaga	cggccccctac	480
cgaaaagcgg	atagacgacc	actttccaaa	aagaaagaag	gctcggaccg	aagaggactc	540
caagccttcc	acctcgtag	acgccgaagc	tggaccacgc	ggatcccagc	agctgcaaat	600
cccagcccaa	ccagcctcaa	gtttgggagc	tgatacaatg	tctgcggggag	gtggcggccc	660
attgggcgac	aataaccaag	gtgccgatgg	agtgggcaat	gcctcggggag	attggcattg	720
cgattccacg	tggatggggg	acagagtcgt	caccaagtcc	acccgaacct	gggtgctgcc	780
cagctacaac	aaccaccagt	accgagagat	caaaagcggc	tccgtcgacg	gaagcaacgc	840
caacgcctac	tttggataca	gcacccccctg	gggggtacttt	gactttaacc	gcttccacag	900
ccactggagc	ccccgagact	ggcaaagact	catcaacaac	tactgggggt	tcagaccccg	960
gtccctcaga	gtcaaaatct	tcaacattca	agtcaaagag	gtcacgggtgc	aggactccac	1020
caccaccatc	gccaacaacc	tcacctccac	cgtcccagtg	tttacggacg	acgactacca	1080
gctgccctac	gtcgtcgga	acgggaccga	gggatgcctg	ccggccttcc	ctccgcaggt	1140
ctttacgctg	ccgcagtagc	gttacgcgac	gctgaaccgc	gacaacacag	aaaatcccac	1200
cgagaggagc	agcttcttct	gcctagagta	ctttcccagc	aagatgctga	gaacgggcaa	1260
caactttgag	tttacctaca	actttgagga	ggtgcccttc	cactccagct	tcgctcccag	1320
tcagaacctg	ttcaagctgg	ccaacccgct	ggtggaccag	tacttgtagc	gcttcgtgag	1380
cacaaataac	actggcggag	tccagttcaa	caagaacctg	gccggggagat	acgccaacac	1440
ctacaaaaac	tgggttcccgg	ggcccatggg	ccgaaccag	ggctggaacc	tgggtcccgg	1500

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ggtcaaccgc	gccagtgtca	ggcgccttcgc	cacgaccaat	aggatggagc	tcgagggcgc	1560
gagttaccag	gtgccccgc	agccgaacgg	catgaccaac	aacctccagg	gcagcaaacac	1620
ctatgccctg	gagaacacta	tgatcttcaa	cagccagccg	gcgaaccggg	gcaccaccgc	1680
cacgtacctc	gagggcaaca	tgctcatcac	cagcgagagc	gagacgcagc	cgggtgaaccg	1740
cgtggcgtag	aacgtcggcg	ggcagatggc	caccaacaac	cagagctcca	ccactgcccc	1800
cgcgaccggc	acgtacaacc	tccaggaaat	cgtgcccggc	agcgtgtgga	tggagaggga	1860
cgtgtacctc	caaggaccca	tctgggcca	gatcccagag	acggggggcg	actttcacc	1920
ctctccggcc	atggggcgat	tccgactcaa	acaccaccg	cccattgatgc	tcattcaagaa	1980
cacgcctgtg	cccggaaata	tcaccagctt	ctcggacgtg	cccgtcagca	gcttcatcac	2040
ccagtacagc	accggggcagg	tcaccgtgga	gatggagtgg	gagctcaaga	aggaaaactc	2100
caagagggtg	aacccagaga	tccagtacac	aaacaactac	aacgaccccc	agttttgtgga	2160
ctttgccccg	gacagcaccg	gggaatacag	aaccaccaga	cctatcggaa	cccgatacct	2220
taccgcaccc	ctttaaccca	tccatgtcgc	ataccctcaa	taaa		2264

<210> 10
 <211> 1292
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/Note =
 synthetic construct

<400> 10						
agcgcaaacg	gctcgtcgcg	cagttttctgg	cagaatcctc	gcagcgctcg	caggaggcgg	60
cttcgcagcg	tgagttctcg	gctgaccggg	tcattcaaaag	caagacttcc	cagaaataca	120
tggcgctcgt	caactggctc	gtggagcagc	gcattcacttc	cgagaagcag	tggatccagg	180
aaaatcagga	gagctacctc	tccttcaact	ccaccggcaa	ctctcggagc	cagatcaagg	240
ccgcgctcga	caacgcgacc	aaaattatga	gtctgacaaa	aagcgcggtg	gactacctcg	300
tggggagctc	cgttcccagc	gacatttcaa	aaaacagaat	ctggcaaatt	tttgagatga	360
atggctacga	cccggcctac	gcgggatcca	tcctctacgg	ctgggtgtcag	cgctccttca	420
acaagaggaa	caccgtctgg	ctctacggac	ccgccacgac	cggcaagacc	aacatcgagg	480
aggccatcgc	ccacactgtg	ccctttttacg	gctgcgtgaa	ctggaccaat	gaaaactttc	540
cctttaatga	ctgtgtggac	aaaatgctca	tttggtggga	ggagggaaag	atgaccaaca	600
aggtgggtga	atccgccaaag	gccatcctgg	ggggtcctaaa	ggtgcgggtc	gatcagaaat	660
gtaaatcctc	tgttcaaat	gattctaccc	ctgtcattgt	aacttccaat	acaaacatgt	720
gtgtgggtgg	ggatgggaat	tccacgacct	ttgaacacca	gcagccgctg	gaggaccgca	780
tgttcaaat	tgaactgact	aagcggtccc	cgccagattt	tggcaagatt	actaagcagg	840
aagtcaagga	cttttttctg	tgggcaaagg	tcaatcaggt	gcccgtgact	cacgagttta	900
aagttcccag	ggaattggcg	ggaactaaag	ggcgaggaga	atctctaaaa	cggccactgg	960
gtgacgtcac	caatactagc	tataaaagtc	tggagaagcg	ggccaggctc	tcatttgttc	1020
ccgagacgcc	tcgcagttca	gacgtgactg	ttgatcccg	tcctctgcga	ccgctcaatt	1080
ggaattcaag	gtatgattgc	aaatgtgact	atcatgtctc	atttgacaac	atttctaaca	1140
aatgtgatga	atgtgaatat	ttgaatcggg	gcaaaaatgg	atgtatctgt	cacaatgtaa	1200
ctcactgtca	aattttgtcat	gggattcccc	cctgggaaaa	ggaaaacttg	tcagattttg	1260
gggattttga	cgatgccaat	aaagaacagt	aa			1292

<210> 11
 <211> 1870
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/Note =
 synthetic construct

<400> 11						
attcttttct	ctggactgct	agaggacct	cgctgccatg	gtacacctct	atgaagtcac	60
tggttcgcgtc	ccattttgacg	tggaggaaca	tctgcttgga	atttctgaca	gctttgtgga	120
ctgggtaact	ggtcaaattt	gggagctgcc	tccagagtca	gatttaaatt	tgactctggg	180
tgaacagcct	cagttgacgg	tggctgatag	aattcgccgc	gtgttcctgt	acgagtggaa	240

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caaat	ttttcc	aagcaggagt	ccaaattc	tt	tgtgcagttt	gaaaagggat	ctgaatat	tt	300
tcattc	gtgcac	acgctt	gttg	agacctcc	gg	atggtcctcg	gccgctac	gt	360
gagtcag	att	cgcgccc	agc	tggtgaa	agt	gggaattgaac	cccagatcaa		420
cgactgg	gtc	gccatcac	ca	aggtaa	agaa	gggaggagcc	aataaggtgg	tggattctgg	480
gtatat	ttccc	gcctacct	gc	tgccga	aggt	ccaaccggag	cttcagtggg	cgtggacaaa	540
cctggac	gag	tataaatt	gg	ccgccct	gaa	tctggaggag	cgcaaaccggc	tcgtcgcgca	600
gtttctg	gca	gaatcctc	gc	agcgctc	gca	ggaggcggct	tcgcagcgtg	agttctcggc	660
tgacctg	gtc	atcaaaa	gca	agacttccc	a	gaaatacatg	gcgctcgtca	actggctcgt	720
ggagcac	ggc	atcacttcc	g	agaagcag	t	gatccaggaa	aatcaggaga	gctacctctc	780
cttcaact	cc	accggcaact		ctcggagcca		gatcaaggcc	gcgctcgaca	acgcgaccaa	840
aattatg	agt	ctgacaaaa		gcgcgggtgga		ctacctcgtg	gggagctccg	ttcccaggga	900
cattttca	aaa	aacagaatct		ggcaaatttt		tgagatgaat	ggctacgacc	cggcctacgc	960
gggatcc	atc	ctctacggct		ggtgtcagcg		ctccttcaac	aagaggaaca	ccgtctggct	1020
ctacggac	ccc	gccacgaccg		gcaagaccaa		catcgcgagg	gccatcgccc	acactgtgcc	1080
cttttac	ggc	tgcgatga	act	ggaccaatga		aaactttccc	tttaatgact	gtgtggacaa	1140
aatgctc	att	gggtgggagg		agggaaagat		gaccaacaag	gtggttgaat	ccgccaaggc	1200
catcctg	ggg	ggctcaaa	agg	tgcgggctga		tcagaaatgt	aaatcctctg	ttcaaattga	1260
ttctaccc	ct	gtcattgtaa		cttccaatac		aaacatgtgt	gtggtgggtg	atgggaattc	1320
cacgacct	ttt	gaacaccagc		agccgctgga		ggaccgcatg	ttcaaatttg	aactgactaa	1380
gcggctccc	g	ccagattttg		gcaagattac		taagcaggaa	gtcaaggact	tttttgcttg	1440
ggcaaa	ggc	aatcagggtg		cggtgactca		cgagttttaa	gttcccaggg	aattggcggg	1500
aactaaa	ggg	gcggagaaat		ctctaaaacg		cccactgggt	gacgtcacca	atactagcta	1560
taaaagt	ctg	gagaagcggg		ccaggctctc		atttgttccc	gagacgcctc	gcagttcaga	1620
cgtgact	gtt	gatccccgctc		ctctgcgacc		gctcaattgg	aattcaagggt	atgattgcaa	1680
atgtgact	at	catgctcaat		ttgacaacat		ttctaacaaa	tgtgatgaat	gtgaatat	1740
gaatcg	gggc	aaaaatggat		gtatctgtca		caatgtaact	cactgtcaaa	tttgtcatgg	1800
gattcccc	c	tgggaaaagg		aaaacttgctc		agattttggg	gattttgacg	atgccataa	1860
agaacag	ttaa								1870

<210> 12

<211> 330

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 12

Met	Ala	Leu	Val	Asn	Trp	Leu	Val	Glu	His	Gly	Ile	Thr	Ser	Glu	Lys
1				5					10					15	
Gln	Trp	Ile	Gln	Glu	Asn	Gln	Glu	Ser	Tyr	Leu	Ser	Phe	Asn	Ser	Thr
			20					25					30		
Gly	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Thr	Lys
		35					40					45			
Ile	Met	Ser	Leu	Thr	Lys	Ser	Ala	Val	Asp	Tyr	Leu	Val	Gly	Ser	Ser
	50				55						60				
Val	Pro	Glu	Asp	Ile	Ser	Lys	Asn	Arg	Ile	Trp	Gln	Ile	Phe	Glu	Met
65				70					75					80	
Asn	Gly	Tyr	Asp	Pro	Ala	Tyr	Ala	Gly	Ser	Ile	Leu	Tyr	Gly	Trp	Cys
			85					90					95		
Gln	Arg	Ser	Phe	Asn	Lys	Arg	Asn	Thr	Val	Trp	Leu	Tyr	Gly	Pro	Ala
			100					105					110		
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
		115					120					125			
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
	130					135					140				
Cys	Val	Asp	Lys	Met	Leu	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Asn
145					150					155				160	
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
				165					170					175	

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Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Val	Gln	Ile	Asp	Ser	Thr	Pro	Val
			180					185					190		
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Val	Val	Val	Asp	Gly	Asn	Ser
		195					200					205			
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Glu	Asp	Arg	Met	Phe	Lys	Phe
		210				215					220				
Glu	Leu	Thr	Lys	Arg	Leu	Pro	Pro	Asp	Phe	Gly	Lys	Ile	Thr	Lys	Gln
225					230					235					240
Glu	Val	Lys	Asp	Phe	Phe	Ala	Trp	Ala	Lys	Val	Asn	Gln	Val	Pro	Val
				245					250					255	
Thr	His	Glu	Phe	Lys	Val	Pro	Arg	Glu	Leu	Ala	Gly	Thr	Lys	Gly	Ala
			260					265					270		
Glu	Lys	Ser	Leu	Lys	Arg	Pro	Leu	Gly	Asp	Val	Thr	Asn	Thr	Ser	Tyr
		275				280						285			
Lys	Ser	Leu	Glu	Lys	Arg	Ala	Arg	Leu	Ser	Phe	Val	Pro	Glu	Thr	Pro
	290					295					300				
Arg	Ser	Ser	Asp	Val	Thr	Val	Asp	Pro	Ala	Pro	Leu	Arg	Pro	Leu	Asn
305					310					315					320
Trp	Asn	Ser	Arg	Leu	Val	Gly	Arg	Ser	Trp						
				325					330						

<210> 13
 <211> 1115
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/Note =
 synthetic construct

<400> 13	
aggagcgc	60
aggagcgc	120
aggagcgc	180
aggagcgc	240
aggagcgc	300
aggagcgc	360
aggagcgc	420
aggagcgc	480
aggagcgc	540
aggagcgc	600
aggagcgc	660
aggagcgc	720
aggagcgc	780
aggagcgc	840
aggagcgc	900
aggagcgc	960
aggagcgc	1020
aggagcgc	1080
aggagcgc	1115

<210> 14
 <211> 550
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/Note =
 synthetic construct

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<400> 14
Met Ala Thr Phe Tyr Glu Val Ile Val Arg Val Pro Phe Asp Val Glu
1 5 10 15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asp Trp Val Thr Gly
20 25 30
Gln Ile Trp Glu Leu Pro Pro Glu Ser Asp Leu Asn Leu Thr Leu Val
35 40 45
Glu Gln Pro Gln Leu Thr Val Ala Asp Arg Ile Arg Arg Val Phe Leu
50 55 60
Tyr Glu Trp Asn Lys Phe Ser Lys Gln Glu Ser Lys Phe Phe Val Gln
65 70 75 80
Phe Glu Lys Gly Ser Glu Tyr Phe His Leu His Thr Leu Val Glu Thr
85 90 95
Ser Gly Ile Ser Ser Met Val Leu Gly Arg Tyr Val Ser Gln Ile Arg
100 105 110
Ala Gln Leu Val Lys Val Val Phe Gln Gly Ile Glu Pro Gln Ile Asn
115 120 125
Asp Trp Val Ala Ile Thr Lys Val Lys Lys Gly Gly Ala Asn Lys Val
130 135 140
Val Asp Ser Gly Tyr Ile Pro Ala Tyr Leu Leu Pro Lys Val Gln Pro
145 150 155 160
Glu Leu Gln Trp Ala Trp Thr Asn Leu Asp Glu Tyr Lys Leu Ala Ala
165 170 175
Leu Asn Leu Glu Glu Arg Lys Arg Leu Val Ala Gln Phe Leu Ala Glu
180 185 190
Ser Ser Gln Arg Ser Gln Glu Ala Ala Ser Gln Arg Glu Phe Ser Ala
195 200 205
Asp Pro Val Ile Lys Ser Lys Thr Ser Gln Lys Tyr Met Ala Leu Val
210 215 220
Asn Trp Leu Val Glu His Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln
225 230 235 240
Glu Asn Gln Glu Ser Tyr Leu Ser Phe Asn Ser Thr Gly Asn Ser Arg
245 250 255
Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Thr Lys Ile Met Ser Leu
260 265 270
Thr Lys Ser Ala Val Asp Tyr Leu Val Gly Ser Ser Val Pro Glu Asp
275 280 285
Ile Ser Lys Asn Arg Ile Trp Gln Ile Phe Glu Met Asn Gly Tyr Asp
290 295 300
Pro Ala Tyr Ala Gly Ser Ile Leu Tyr Gly Trp Cys Gln Arg Ser Phe
305 310 315 320
Asn Lys Arg Asn Thr Val Trp Leu Tyr Gly Pro Ala Thr Thr Gly Lys
325 330 335
Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro Phe Tyr Gly Cys
340 345 350
Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp Cys Val Asp Lys
355 360 365
Met Leu Ile Trp Trp Glu Glu Gly Lys Met Thr Asn Lys Val Val Glu
370 375 380
Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg Val Asp Gln Lys
385 390 395 400
Cys Lys Ser Ser Val Gln Ile Asp Ser Thr Pro Val Ile Val Thr Ser
405 410 415
Asn Thr Asn Met Cys Val Val Val Asp Gly Asn Ser Thr Thr Phe Glu
420 425 430
His Gln Gln Pro Leu Glu Asp Arg Met Phe Lys Phe Glu Leu Thr Lys
435 440 445
Arg Leu Pro Pro Asp Phe Gly Lys Ile Thr Lys Gln Glu Val Lys Asp
450 455 460
Phe Phe Ala Trp Ala Lys Val Asn Gln Val Pro Val Thr His Glu Phe
465 470 475 480

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Lys Val Pro Arg Glu Leu Ala Gly Thr Lys Gly Ala Glu Lys Ser Leu
 485 490 495
 Lys Arg Pro Leu Gly Asp Val Thr Asn Thr Ser Tyr Lys Ser Leu Glu
 500 505 510
 Lys Arg Ala Arg Leu Ser Phe Val Pro Glu Thr Pro Arg Ser Ser Asp
 515 520 525
 Val Thr Val Asp Pro Ala Pro Leu Arg Pro Leu Asn Trp Asn Ser Arg
 530 535 540
 Leu Val Gly Arg Ser Trp
 545 550

<210> 15
 <211> 1690
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/Note =
 synthetic construct

<400> 15
 attctttgct ctggactgct agaggaccct cgtgccatg gctaccttct atgaagtcac 60
 tggtcgcgtc ccatttgacg tggaggaaca tctgcctgga atttctgaca gctttgtgga 120
 ctgggtaact ggtcaaattt gggagctgcc tccagagtca gatttaaatt tgactctggt 180
 tgaacagcct cagttgacgg tggctgatag aattcgccgc gtgttctgt acgagtggaa 240
 caaattttcc aagcaggagt ccaaattctt tgtgcagttt gaaaagggat ctgaatatatt 300
 tcatctgcac acgcttgtgg agacctccgg catctcttcc atgggtctcg gccgctacgt 360
 gagtcagatt cgcgcccagc tggtgaaagt ggtcttccag ggaattgaac cccagatcaa 420
 cgactgggtc gccatcacca aggtaaagaa gggcggagcc aataagggtg tggattctgg 480
 gtatatcccg gcctacctgc tgccgaaggt ccaaccggag cttcagtggg cgtggacaaa 540
 cctggacgag tataaattgg ccgccctgaa tctggaggag cgcaaaccgg tcgtcgcgca 600
 gtttctggca gaatctctgc agcgctcgca ggaggcggct tcgcagcgtg agttctcggc 660
 tgaccgggtc atcaaaaagca agacttccca gaaatacatg gcgctcgtca actggctcgt 720
 ggagcacggc atcaactccg agaagcagtg gatccaggaa aatcaggaga gctacctctc 780
 cttcaactcc accggcaact ctcgagacca gatcaaggcc gcgctcgaca acgcgaccaa 840
 aattatgagt ctgacaaaaa gcgcgggtgga ctacctcgtg gggagctccg ttcccaggga 900
 catttcaaaa aacagaatct ggcaaatttt tgagatgaat ggctacgacc cggcctacgc 960
 gggatccatc ctctacgggt ggtgtcagcg ctccttcaac aagaggaaca ccgtctggct 1020
 ctacggaccc gccacgaccg gcaagaccaa catcgcgag gccatcgccc acactgtgcc 1080
 cttttacggc tgcgtgaact ggaccaatga aaactttccc tttaatgact gtgtggacaa 1140
 aatgctcatt tgggtgggagg agggaaagat gaccaacaag gtggttgaat ccgccaaggc 1200
 catcctgggg ggctcaaagg tgcgggtcga tcagaaatgt aaatcctctg ttcaaattga 1260
 ttctaccctt gtcattgtaa ctccaatac aaacatgtgt gtggtggtgg atgggaattc 1320
 cacgaccttt gaacaccagc agccgctgga ggaccgcatg ttcaaatttg aactgactaa 1380
 gcggctcccg ccagattttg gcaagattac taagcaggaa gtcaaggact tttttgcttg 1440
 ggcaaaggtc aatcaggtgc cggtgactca cgagtttaaa gttcccaggg aattggcggg 1500
 aactaaaggg gcggagaaat ctctaaaacg cccactgggt gacgtcacca atactagcta 1560
 taaaagtctg gagaagcggg ccaggctctc atttgttccc gagacgcctc gcagttcaga 1620
 cgtgactggt gatcccgctc ctctgcgacc gctcaattgg aattcaagat tggttggaag 1680
 aagttggtga 1690

<210> 16
 <211> 145
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/Note =
 synthetic construct

<400> 16
 ccatcaccaa ggtaaagaag ggcggagcca ataaggtggt ggattctggg tatattcccg 60

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cctacctgct gccgaaggtc caaccggagc ttcagtgggc gtggacaaac ctggacgagt 120
ataaattggc cgccctgaat ctgga 145

<210> 17
<211> 174
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 17
taagcaggaa gtcaaggact tttttgcttg ggcaaaggtc aatcagggtc cggtgactca 60
cgagtttaaa gttcccaggg aattggcggg aactaaaggg gcggagaaat ctctaaaacg 120
cccactgggt gacgtcacca atactagcta taaaagtctg gagaagcggg ccag 174

<210> 18
<211> 187
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 18
cactctcaag caaggggggtt ttgtaagcag tgatgtcata atgatgtaat gcttattgtc 60
acgcgatagt taatgattaa cagtcagtgt atgtgtttta tccaatagga agaaagcgcg 120
cgtatgagt ctcgcgagac ttccggggta taaaagaccg agtgaacgag cccgccgcca 180
ttctttg 187

<210> 19
<211> 168
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 19
aaacctcctt gcttgagagt gtggcactct cccccctgtc gcgttcgctc gctcgctggc 60
tcgtttgggg ggggtggcagc tcaaagagct gccagacgac ggccctcttg ccgtcgcccc 120
cccaaacgag ccagcgagcg agcgaacgag acagggggga gagtgcc 168

<210> 20
<211> 168
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 20
aaacctcctt gcttgagagt gtggcactct cccccctgtc gcgttcgctc gctcgctggc 60
tcgtttgggg gggcgacggc cagagggcgg tcgtctgccc gctctttgag ctgccacccc 120
cccaaacgag ccagcgagcg agcgaacgag acagggggga gagtgcc 168

<210> 21

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<211> 8
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
        synthetic construct

<400> 21
cgggtgtga                                     8

<210> 22
<211> 8
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
        synthetic construct

<400> 22
cgggttgag                                     8

<210> 23
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
        synthetic construct

<400> 23
caaaacctcc ttgcttgaga g                     21

<210> 24
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
        synthetic construct

<400> 24
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu
 1          5          10          15
Ser Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro
 20          25          30
Pro Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu
 35          40          45
Pro Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu
 50          55          60
Pro Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr
 65          70          75          80
Asp Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His
 85          90          95
Ala Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly
100          105          110

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Gly	Asn	Leu	Gly	Arg	Ala	Val	Phe	Gln	Ala	Lys	Lys	Arg	Val	Leu	Glu	
		115					120					125				
Pro	Leu	Gly	Leu	Val	Glu	Glu	Pro	Val	Lys	Thr	Ala	Pro	Gly	Lys	Lys	
	130					135					140					
Arg	Pro	Val	Glu	His	Ser	Pro	Val	Glu	Pro	Asp	Ser	Ser	Ser	Gly	Thr	
	145				150					155					160	
Gly	Lys	Ala	Gly	Gln	Gln	Pro	Ala	Arg	Lys	Arg	Leu	Asn	Phe	Gly	Gln	
				165					170					175		
Thr	Gly	Asp	Ala	Asp	Ser	Val	Pro	Asp	Pro	Gln	Pro	Leu	Gly	Gln	Pro	
			180					185					190			
Pro	Ala	Ala	Pro	Ser	Gly	Leu	Gly	Thr	Asn	Thr	Met	Ala	Thr	Gly	Ser	
		195					200					205				
Gly	Ala	Pro	Met	Ala	Asp	Asn	Asn	Glu	Gly	Ala	Asp	Gly	Val	Gly	Asn	
	210					215					220					
Ser	Ser	Gly	Asn	Trp	His	Cys	Asp	Ser	Thr	Trp	Met	Gly	Asp	Arg	Val	
	225				230					235					240	
Ile	Thr	Thr	Ser	Thr	Arg	Thr	Trp	Ala	Leu	Pro	Thr	Tyr	Asn	Asn	His	
				245					250					255		
Leu	Tyr	Lys	Gln	Ile	Ser	Ser	Gln	Ser	Gly	Ala	Ser	Asn	Asp	Asn	His	
			260					265					270			
Tyr	Phe	Gly	Tyr	Ser	Thr	Pro	Trp	Gly	Tyr	Phe	Asp	Phe	Asn	Arg	Phe	
		275					280					285				
His	Cys	His	Phe	Ser	Pro	Arg	Asp	Trp	Gln	Arg	Leu	Ile	Asn	Asn	Asn	
	290					295					300					
Trp	Gly	Phe	Arg	Pro	Lys	Arg	Leu	Asn	Phe	Lys	Leu	Phe	Asn	Ile	Gln	
	305				310					315					320	
Val	Lys	Glu	Val	Thr	Gln	Asn	Asp	Gly	Thr	Thr	Thr	Ile	Ala	Asn	Asn	
				325					330					335		
Leu	Thr	Ser	Thr	Val	Gln	Val	Phe	Thr	Asp	Ser	Glu	Tyr	Gln	Leu	Pro	
			340					345					350			
Tyr	Val	Leu	Gly	Ser	Ala	His	Gln	Gly	Cys	Leu	Pro	Pro	Phe	Pro	Ala	
		355					360					365				
Asp	Val	Phe	Met	Val	Pro	Gln	Tyr	Gly	Tyr	Leu	Thr	Leu	Asn	Asn	Gly	
	370					375					380					
Ser	Gln	Ala	Val	Gly	Arg	Ser	Ser	Phe	Tyr	Cys	Leu	Glu	Tyr	Phe	Pro	
	385				390					395					400	
Ser	Gln	Met	Leu	Arg	Thr	Gly	Asn	Asn	Phe	Thr	Phe	Ser	Tyr	Thr	Phe	
				405					410					415		
Glu	Asp	Val	Pro	Phe	His	Ser	Ser	Tyr	Ala	His	Ser	Gln	Ser	Leu	Asp	
			420					425					430			
Arg	Leu	Met	Asn	Pro	Leu	Ile	Asp	Gln	Tyr	Leu	Tyr	Tyr	Leu	Ser	Arg	
		435					440					445				
Thr	Asn	Thr	Pro	Ser	Gly	Thr	Thr	Thr	Gln	Ser	Arg	Leu	Gln	Phe	Ser	
	450					455					460					
Gln	Ala	Gly	Ala	Ser	Asp	Ile	Arg	Asp	Gln	Ser	Arg	Asn	Trp	Leu	Pro	
	465				470					475					480	
Gly	Pro	Cys	Tyr	Arg	Gln	Gln	Arg	Val	Ser	Lys	Thr	Ser	Ala	Asp	Asn	
				485					490					495		
Asn	Asn	Ser	Glu	Tyr	Ser	Trp	Thr	Gly	Ala	Thr	Lys	Tyr	His	Leu	Asn	Gly
			500					505					510			
Arg	Asp	Ser	Leu	Val	Asn	Pro	Gly	Pro	Ala	Met	Ala	Ser	His	Lys	Asp	
		515					520					525				
Asp	Glu	Glu	Lys	Phe	Phe	Pro	Gln	Ser	Gly	Val	Leu	Ile	Phe	Gly	Lys	
	530					535					540					
Gln	Gly	Ser	Glu	Lys	Thr	Asn	Val	Asp	Ile	Glu	Lys	Val	Met	Ile	Thr	
	545				550					555					560	
Asp	Glu	Glu	Glu	Ile	Arg	Thr	Thr	Asn	Pro	Val	Ala	Thr	Glu	Gln	Tyr	
				565					570					575		
Gly	Ser	Val	Ser	Thr	Asn	Leu	Gln	Arg	Gly	Asn	Arg	Gln	Ala	Ala	Thr	
			580					585					590			

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Ala	Asp	Val	Asn	Thr	Gln	Gly	Val	Leu	Pro	Gly	Met	Val	Trp	Gln	Asp
		595					600					605			
Arg	Asp	Val	Tyr	Leu	Gln	Gly	Pro	Ile	Trp	Ala	Lys	Ile	Pro	His	Thr
	610					615					620				
Asp	Gly	His	Phe	His	Pro	Ser	Pro	Leu	Met	Gly	Gly	Phe	Gly	Leu	Lys
	625				630					635					640
His	Pro	Pro	Pro	Gln	Ile	Leu	Ile	Lys	Asn	Thr	Pro	Val	Pro	Ala	Asn
				645					650					655	
Pro	Ser	Thr	Thr	Phe	Ser	Ala	Ala	Lys	Phe	Ala	Ser	Phe	Ile	Thr	Gln
			660					665					670		
Tyr	Ser	Thr	Gly	Gln	Val	Ser	Val	Glu	Ile	Glu	Trp	Glu	Leu	Gln	Lys
		675					680					685			
Glu	Asn	Ser	Lys	Arg	Trp	Asn	Pro	Glu	Ile	Gln	Tyr	Thr	Ser	Asn	Tyr
	690					695					700				
Asn	Lys	Ser	Val	Asn	Val	Asp	Phe	Thr	Val	Asp	Thr	Asn	Gly	Val	Tyr
	705				710					715					720
Ser	Glu	Pro	Arg	Pro	Ile	Gly	Thr	Arg	Tyr	Leu	Thr	Arg	Asn	Leu	
				725					730					735	

B.
cancel